QTL AND CANDIDATE GENES FOR GROWTH TRAITS IN PINUS TAEDA
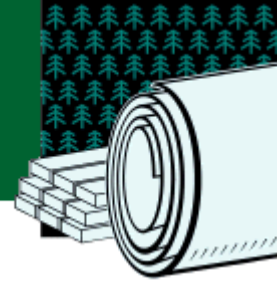
BENEFITS

- Increases the efficiency of genetic improvement programs
- Raises the volume of wood grown per acre in the southern United States
- Bridges genetic and physical maps by LC-SSR clustering, being proximal to or inside protein coding regions
- Adds new information of genome architecture and gene expression

APPLICATIONS

If the results of this study are positive, many forest product companies will conduct pilot scale tests because the mapping pedigree is associated with the best genetic material available today. These results would also be used for selection or breeding if genes for growth can be identified at seedling and older stages.

Alternative QTL Analysis to Identify Candidate Genes for Growth

Although conventional quantitative trait loci (QTL) analysis uses markers linked to QTL in older tree traits, it has only been used for seedling measurement. For this project, researchers will examine an alternative QTL analysis that will identify candidate genes for growth at the seedling stage and at older ages using three new methods: low-copy SSR (LC-SSR) markers; candidate gene detection step; and a study of older-tree traits in an extended pedigree.

LC-SSR markers, in the low-copy portion of the genome, are both codominant and highly polymorphic. Five markers, linked or inside candidate genes, will be tested for correlation with seedling and older-tree growth traits. The candidate gene detection step was added to speed up identification of LC-SSR markers; a prototype candidate gene was found to have a phenotypic effect on early vigor and development. 13 years worth of age data and DNA samples provided by Texas A & M will be used for a conventional QTL analysis to complement the study's candidate gene effort. Positive conclusions from this project could affect genetic engineering projects designed to increase wood quantity and quality.
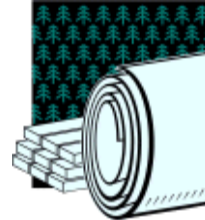
PROJECT DESCRIPTION

Goal: To conduct a novel, alternative QTL analysis that will identify growth traits in Pinus taeda using LC-SSR markers, candidate gene detection and older-tree traits in an extended pedigree

Major tasks for this three year project are outlined below:

1. Develop LC-SSR markers (during the first and second year)

2. Relate candidate genes to seedling and older-tree growth traits

3. Conduct QTL analysis with 100 informative LC-SSRs on 200 progeny in the seedling cohort and 100 progeny in the older-tree cohort

PROGRESS & MILESTONES

- Researchers from Texas A & M University developed molecular marker, low-copy microsatellites (LC-SSRs), which are codominant and highly polymorphic.
- Screening of self progeny revealed five markers proximal to or inside candidate genes that will be tested.
- Eighteen polymorphic markers were released for public use and others will be released after December 31, 2000.
- The prototype candidate gene screening revealed that allele A had a changed protein structured due to addition of two glutamine residues and allele B had premature termination codon towards the 3' end.
- All phenotypic age data and DNA data was collected by Texas A & M University for the QTL study for assessing the relationship between candidate genes and mature-tree phenotypes over the last 13 years.